

Title: US-09-873-829-1  
Perfect score: 1823  
Sequence: 1 CAGATGGATCCTAATAGAAT.....GTACAAAAGTCGACGGCCGC 1823

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	1823	100.0	1823	9	AF013171		AF013171 Homo sapi
2	1770.6	97.1	2226	6	AX695690		AX695690 Sequence
3	1770.6	97.1	2271	6	BD231044		BD231044 Method fo
4	1770.6	97.1	2271	6	AR429486		AR429486 Sequence
5	1770.6	97.1	2271	6	AX664282		AX664282 Sequence
6	1770.6	97.1	2271	9	AF053712		AF053712 Homo sapi
7	1770.6	97.1	2274	6	BD096827		BD096827 Osteoprot
8	1755.4	96.3	2390	6	AX201362		AX201362 Sequence
9	1754.8	96.3	2201	9	AF019047		AF019047 Homo sapi
10	1456	79.9	52754	6	AX695689		AX695689 Sequence
c 11	1454.4	79.8	200724	9	AL139382		AL139382 Human DNA
c 12	1222.2	67.0	113451	2	AC023297		AC023297 Homo sapi
13	1000	54.9	2225	10	AF019048		AF019048 Mus muscu
14	998.4	54.8	2295	6	AR062119		AR062119 Sequence

15	998.4	54.8	2295	6	BD096826	BD096826 Osteoprot
16	998.4	54.8	2299	6	BD231046	BD231046 Method fo
17	998.4	54.8	2299	6	AR429488	AR429488 Sequence
18	998.4	54.8	2299	10	AF053713	AF053713 Mus muscu
19	977.2	53.6	1561	9	BC040889	BC040889 Homo sapi
20	971	53.3	2237	6	AX695687	AX695687 Sequence
21	971	53.3	2237	10	AF013170	AF013170 Mus muscu
22	957.2	52.5	2191	6	AR157058	AR157058 Sequence
23	957.2	52.5	2191	6	AX140162	AX140162 Sequence
24	957.2	52.5	2191	6	BD064044	BD064044 Mammalian
25	834.2	45.8	930	9	AB037599	AB037599 Homo sapi
26	832.8	45.7	1630	6	AR156433	AR156433 Sequence
27	832.8	45.7	1630	6	AR164147	AR164147 Sequence
28	832.8	45.7	1630	6	BD132527	BD132527 Ligand fo
29	832.8	45.7	1630	6	BD132533	BD132533 Receptor
30	832.8	45.7	1630	6	AR218281	AR218281 Sequence
31	832.8	45.7	1630	6	AR254110	AR254110 Sequence
32	832.8	45.7	1630	6	AR285409	AR285409 Sequence
33	832.8	45.7	1630	6	AR300118	AR300118 Sequence
34	832.8	45.7	1630	6	AR317338	AR317338 Sequence
35	832.8	45.7	1630	6	AR430236	AR430236 Sequence
36	832.8	45.7	1630	6	AX147987	AX147987 Sequence
37	832.8	45.7	1694	6	AX451897	AX451897 Sequence
38	806.2	44.2	52479	6	AX695686	AX695686 Sequence
39	806.2	44.2	214499	2	AC126690	AC126690 Mus muscu
40	779	42.7	2029	6	E34349	E34349 DNA and pro
41	779	42.7	2029	10	AB022036S4	AB022039 Mus muscu
42	757	41.5	274587	2	AC094149	AC094149 Rattus no
43	752.2	41.3	1003	9	BC074823	BC074823 Homo sapi
44	752.2	41.3	1003	9	BC074890	BC074890 Homo sapi
45	733.2	40.2	818	9	AB064268	AB064268 Homo sapi

Title: US-09-873-829-1  
Perfect score: 1823  
Sequence: 1 CAGATGGATCCTAATAGAAT.....GTACAAAAGTCGACGGCCGC 1823

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1823	100.0	1823	2	AAX80223	Aax80223 Human TRA
2	1823	100.0	1823	8	ABX94284	Abx94284 cDNA enco
3	1823	100.0	1823	8	ACC57900	Acc57900 Human RAN
4	1823	100.0	1823	10	ACC57571	Acc57571 Human RAN
5	1770.6	97.1	1945	6	ABK12877	Abk12877 cDNA enco
6	1770.6	97.1	2226	6	ABK12876	Abk12876 cDNA enco
7	1770.6	97.1	2226	9	ADA02799	Ada02799 Human TNF
8	1770.6	97.1	2226	10	ADB72537	Adb72537 Human TNF
9	1770.6	97.1	2226	10	ADC85279	Adc85279 Human Tnf
10	1770.6	97.1	2226	12	ADM74394	Adm74394 Human car
11	1770.6	97.1	2271	3	AAZ99964	Aaz99964 DNA encod
12	1770.6	97.1	2271	10	ADC35203	Adc35203 Human cDN
13	1770.6	97.1	2271	10	AAD63913	Aad63913 Human RAN
14	1770.6	97.1	2271	10	ABV75842	Abv75842 Human ost
15	1770.6	97.1	2274	2	AAV70285	Aav70285 Human ost

16	1769	97.0	1931	12	ADO19773	Ado19773 Human PRO
17	1755.4	96.3	2390	6	ABK40274	Abk40274 cDNA enco
18	1755.4	96.3	2390	10	ADJ37322	Adj37322 Human tum
19	1755.4	96.3	2390	12	ADG68246	Adg68246 Human PRO
20	1754.8	96.3	2201	10	ACC57572	Acc57572 Human RAN
21	1754.8	96.3	2201	13	ADT08154	Adt08154 Human RAN
22	1456	79.9	52754	9	ADA02798	Ada02798 Human TNF
23	1456	79.9	52754	10	ADB72536	Adb72536 Human TNF
24	1456	79.9	52754	10	ADC85278	Adc85278 Human Tnf
25	1456	79.9	52754	12	ADM74393	Adm74393 Human car
26	1000	54.9	2225	13	ADT08152	Adt08152 Murine RA
27	998.4	54.8	2295	2	AAV70284	Aav70284 Human ost
28	998.4	54.8	2299	3	AAZ99966	Aaz99966 DNA encod
29	971	53.3	2237	2	AAX80224	Aax80224 Murine TR
30	971	53.3	2237	6	ABK12880	Abk12880 cDNA enco
31	971	53.3	2237	8	ABX94285	Abx94285 cDNA enco
32	971	53.3	2237	9	ADA02796	Ada02796 Mouse Tnf
33	971	53.3	2237	10	ADB72534	Adb72534 Mouse Tnf
34	971	53.3	2237	10	ADC85276	Adc85276 Mouse Tnf
35	971	53.3	2237	12	ADM74391	Adm74391 Murine ca
36	957.2	52.5	2191	2	AAV41489	Aav41489 Nucleotid
37	834.2	45.8	930	10	ADC78864	Adc78864 Human PRO
38	832.8	45.7	1630	2	AAV41377	Aav41377 NF-kB rec
39	832.8	45.7	1630	2	AAV41371	Aav41371 NF-kB rec
40	832.8	45.7	1630	2	AAD15310	Aad15310 Murine re
41	832.8	45.7	1630	4	AAD08714	Aad08714 Murine re
42	832.8	45.7	1630	4	AAD05903	Aad05903 Murine RA
43	832.8	45.7	1630	6	AAD43212	Aad43212 Mouse RAN
44	832.8	45.7	1630	9	ADB16985	Adb16985 Murine re
45	832.8	45.7	1630	10	ADC72999	Adc72999 Murine RA

Title: US-09-873-829-1  
Perfect score: 1823  
Sequence: 1 CAGATGGATCCTAATAGAAT.....GTACAAAAGTCGACGGCCGC 1823

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	1770.6	97.1	2271	3	US-09-052-521C-3	Sequence 3, Appli
2	1770.6	97.1	2271	4	US-09-396-937-1	Sequence 1, Appli
3	998.4	54.8	2295	2	US-08-842-842-6	Sequence 6, Appli
4	998.4	54.8	2295	3	US-09-052-521C-1	Sequence 1, Appli
5	998.4	54.8	2299	4	US-09-396-937-5	Sequence 5, Appli
6	957.2	52.5	2191	3	US-08-989-362-1	Sequence 1, Appli
7	957.2	52.5	2191	4	US-09-671-658A-1	Sequence 1, Appli
8	832.8	45.7	1630	3	US-08-996-139-10	Sequence 10, Appli
9	832.8	45.7	1630	3	US-08-995-659-10	Sequence 10, Appli
10	832.8	45.7	1630	3	US-09-215-649A-10	Sequence 10, Appli
11	832.8	45.7	1630	3	US-09-577-780-10	Sequence 10, Appli
12	832.8	45.7	1630	4	US-09-577-800-10	Sequence 10, Appli
13	832.8	45.7	1630	4	US-09-466-496-10	Sequence 10, Appli
14	832.8	45.7	1630	4	US-09-871-856-10	Sequence 10, Appli
15	832.8	45.7	1630	4	US-09-871-291-10	Sequence 10, Appli
16	832.8	45.7	1630	4	US-09-877-650-10	Sequence 10, Appli
17	832.8	45.7	1630	4	US-09-865-363-10	Sequence 10, Appli
18	832.8	45.7	1630	4	US-09-688-459-10	Sequence 10, Appli
19	733.2	40.2	954	3	US-08-996-139-12	Sequence 12, Appli
20	733.2	40.2	954	3	US-08-995-659-12	Sequence 12, Appli
21	733.2	40.2	954	3	US-09-215-649A-12	Sequence 12, Appli
22	733.2	40.2	954	3	US-09-577-780-12	Sequence 12, Appli

23	733.2	40.2	954	4	US-09-577-800-12	Sequence 12, Appl
24	733.2	40.2	954	4	US-09-466-496-12	Sequence 12, Appl
25	733.2	40.2	954	4	US-09-871-856-12	Sequence 12, Appl
26	733.2	40.2	954	4	US-09-871-291-12	Sequence 12, Appl
27	733.2	40.2	954	4	US-09-877-650-12	Sequence 12, Appl
28	733.2	40.2	954	4	US-09-865-363-12	Sequence 12, Appl
29	733.2	40.2	954	4	US-09-688-459-12	Sequence 12, Appl
30	514.4	28.2	951	4	US-09-396-937-3	Sequence 3, Appli
31	274.8	15.1	564	4	US-09-396-937-7	Sequence 7, Appli
32	274.4	15.1	519	4	US-09-396-937-9	Sequence 9, Appli
33	274.4	15.1	519	4	US-09-396-937-11	Sequence 11, Appl
34	245.6	13.5	519	4	US-09-396-937-17	Sequence 17, Appl
35	229.6	12.6	519	4	US-09-396-937-19	Sequence 19, Appl
36	226.2	12.4	546	4	US-09-396-937-15	Sequence 15, Appl
37	208.2	11.4	564	4	US-09-396-937-13	Sequence 13, Appl
38	69.4	3.8	759	3	US-09-320-424-10	Sequence 10, Appl
39	69.4	3.8	759	4	US-09-825-563-10	Sequence 10, Appl
40	69.4	3.8	768	3	US-09-320-424-12	Sequence 12, Appl
41	69.4	3.8	768	4	US-09-825-563-12	Sequence 12, Appl
42	69.4	3.8	1042	3	US-08-584-031-2	Sequence 2, Appli
43	69.4	3.8	1042	3	US-08-780-496-2	Sequence 2, Appli
44	69.4	3.8	1042	4	US-09-582-450-2	Sequence 2, Appli
45	69.4	3.8	1042	4	US-09-934-465-2	Sequence 2, Appli

Title: US-09-873-829-1  
Perfect score: 1823  
Sequence: 1 CAGATGGATCCTAATAGAAT.....GTACAAAAGTCGACGGCCGC 1823

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PECTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*

17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*

19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*

21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	1823	100.0	1823	10	US-09-873-829-1	Sequence 1, Appli
2	1823	100.0	1823	13	US-10-017-910-1	Sequence 1, Appli
3	1823	100.0	1823	15	US-10-272-411-1	Sequence 1, Appli
4	1823	100.0	1823	15	US-10-272-328A-1	Sequence 1, Appli
5	1823	100.0	1823	17	US-10-202-062-21	Sequence 21, Appli
6	1770.6	97.1	1945	11	US-09-933-915A-9	Sequence 9, Appli

7	1770.6	97.1	2226	11	US-09-997-722-65	Sequence 65, Appl
8	1770.6	97.1	2226	11	US-09-933-915A-1	Sequence 1, Appl
9	1770.6	97.1	2271	15	US-10-218-547-21	Sequence 21, Appl
10	1770.6	97.1	2271	16	US-10-310-793-27	Sequence 27, Appl
11	1770.6	97.1	2271	18	US-10-664-801-1	Sequence 1, Appl
12	1770.6	97.1	2271	18	US-10-825-898-3	Sequence 3, Appl
13	1770.6	97.1	2271	19	US-10-129-595-2	Sequence 2, Appl
14	1755.4	96.3	2390	16	US-10-210-951-41	Sequence 41, Appl
15	1755.4	96.3	2390	16	US-10-211-884-41	Sequence 41, Appl
16	1755.4	96.3	2390	17	US-10-211-858-41	Sequence 41, Appl
17	1754.8	96.3	2201	15	US-10-272-411-51	Sequence 51, Appl
18	1754.8	96.3	2201	15	US-10-272-328A-51	Sequence 51, Appl
19	1754.8	96.3	2201	18	US-10-799-345-11	Sequence 11, Appl
20	1456	79.9	52754	11	US-09-997-722-64	Sequence 64, Appl
21	1000	54.9	2225	18	US-10-799-345-9	Sequence 9, Appl
22	998.4	54.8	2295	10	US-09-079-569-6	Sequence 6, Appl
23	998.4	54.8	2295	18	US-10-825-898-1	Sequence 1, Appl
24	998.4	54.8	2299	18	US-10-664-801-5	Sequence 5, Appl
25	971	53.3	2237	10	US-09-873-829-3	Sequence 3, Appl
26	971	53.3	2237	11	US-09-997-722-62	Sequence 62, Appl
27	971	53.3	2237	11	US-09-933-915A-15	Sequence 15, Appl
28	971	53.3	2237	13	US-10-017-910-3	Sequence 3, Appl
29	957.2	52.5	2191	15	US-10-326-052-1	Sequence 1, Appl
30	832.8	45.7	1630	9	US-09-871-856-10	Sequence 10, Appl
31	832.8	45.7	1630	9	US-09-865-363-10	Sequence 10, Appl
32	832.8	45.7	1630	9	US-09-871-291-10	Sequence 10, Appl
33	832.8	45.7	1630	9	US-09-877-650-10	Sequence 10, Appl
34	832.8	45.7	1630	16	US-10-405-878-10	Sequence 10, Appl
35	832.8	45.7	1630	18	US-10-802-133-10	Sequence 10, Appl
36	832.8	45.7	1694	9	US-09-957-944-7	Sequence 7, Appl
37	806.2	44.2	52479	11	US-09-997-722-61	Sequence 61, Appl
38	733.2	40.2	741	16	US-10-167-182-19	Sequence 19, Appl
39	733.2	40.2	741	17	US-10-460-623-19	Sequence 19, Appl
40	733.2	40.2	741	18	US-10-854-300-19	Sequence 19, Appl
41	733.2	40.2	954	9	US-09-871-856-12	Sequence 12, Appl
42	733.2	40.2	954	9	US-09-957-944-5	Sequence 5, Appl
43	733.2	40.2	954	9	US-09-865-363-12	Sequence 12, Appl
44	733.2	40.2	954	9	US-09-871-291-12	Sequence 12, Appl
45	733.2	40.2	954	9	US-09-877-650-12	Sequence 12, Appl

Title: US-09-873-829-1  
Perfect score: 1823  
Sequence: 1 CAGATGGATCCTAATAGAAT.....GTACAAAAGTCGACGGCCGC 1823

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_htc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	Description
	1	742	40.7	755	5	BX105834	BX105834 BX105834
	2	733.2	40.2	954	9	AY415854	AY415854 Homo sapi
	3	720	39.5	735	9	AY415855	AY415855 Pan trogl
C	4	702.2	38.5	770	5	BQ007726	BQ007726 UI-H-EI0-
	5	554.8	30.4	575	8	AQ417854	AQ417854 RPCI-11-1
	6	494	27.1	951	9	AY415856	AY415856 Mus muscu
C	7	480.2	26.3	539	5	BM893658	BM893658 ij28a04.x
C	8	461.2	25.3	524	8	AQ827122	AQ827122 HS_5256_B
	9	421.6	23.1	670	9	CE649975	CE649975 tigr-gss-
C	10	417.4	22.9	529	8	AQ827168	AQ827168 HS_5256_B
	11	408	22.4	419	1	AA504450	AA504450 aa59h12.r
C	12	391.6	21.5	462	1	AI808584	AI808584 wf56b11.x
C	13	390.8	21.4	612	6	CB480349	CB480349 jns63_A11
C	14	375.4	20.6	694	9	AG319098	AG319098 Mus muscu
C	15	357.4	19.6	612	8	BH267783	BH267783 CH230-186
C	16	342	18.8	725	9	AG484312	AG484312 Mus muscu
C	17	317.2	17.4	375	1	AA504211	AA504211 aa59h12.s
	18	311	17.1	514	2	BE335979	BE335979 us84g09.y
	19	289	15.9	482	2	BE633100	BE633100 uv73a04.y

20	280.2	15.4	530	1	AA170348	AA170348 ms88g11.r	
21	266.2	14.6	362	1	AV653073	AV653073 AV653073	
22	251	13.8	475	2	BB637568	BB637568 BB637568	
23	249.4	13.7	659	9	AG107545	AG107545 Pan trogl	
24	246.4	13.5	462	3	AK041129	AK041129 Mus muscu	
25	244.4	13.4	469	2	BB223942	BB223942 BB223942	
26	229.4	12.6	599	7	CK823311	CK823311 ij28a04.y	
27	224.4	12.3	564	8	BZ925349	BZ925349 CH240_71J	
28	204	11.2	572	5	BM966907	BM966907 ij28a04.y	
29	190.6	10.5	688	6	BY753873	BY753873 BY753873	
30	176.6	9.7	671	6	BY754477	BY754477 BY754477	
31	171.2	9.4	365	6	BY699230	BY699230 BY699230	
32	165	9.1	380	6	BY700342	BY700342 BY700342	
33	162	8.9	413	8	AQ817650	AQ817650 HS_5265_B	
34	153.4	8.4	386	6	BY699584	BY699584 BY699584	
35	153	8.4	345	6	BY692177	BY692177 BY692177	
36	145	8.0	313	2	BB220722	BB220722 BB220722	
c	37	139.8	7.7	580	9	CE705944	CE705944 tigr-gss-
	38	138.8	7.6	306	2	BB240334	BB240334 BB240334
	39	131.6	7.2	671	6	BY753653	BY753653 BY753653
c	40	131.6	7.2	889	5	BX772925	BX772925 BX772925
	41	130.2	7.1	855	5	BX843917	BX843917 BX843917
	42	128	7.0	316	2	BB236029	BB236029 BB236029
	43	123.4	6.8	314	2	BB236016	BB236016 BB236016
	44	117.2	6.4	316	2	BB236026	BB236026 BB236026
	45	112.2	6.2	288	2	BB216722	BB216722 BB216722

Title: US-09-873-829-2  
Perfect score: 1299  
Sequence: 1 QMDPNRISEDGTHCIYRILR.....LLDPDQDATYFGAFKVRDID 245

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp

```
Q=/cgn2_1/USPTO_spool_p/US09873829/runat_10032005_161838_26939/app_query.fasta_1
.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09873829@CGN_1_1_5600@runat_10032005_161838_26939 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

```
Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: qb_vi:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

10

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1299	100.0	1823	9	AF013171	AF013171 Homo sapi
2	1293	99.5	818	9	AB064268	AB064268 Homo sapi
3	1293	99.5	829	6	E50524	E50524 Novel solub
4	1293	99.5	911	9	AB061227	AB061227 Homo sapi
5	1293	99.5	930	9	AB037599	AB037599 Homo sapi
6	1293	99.5	954	6	AR156434	AR156434 Sequence
7	1293	99.5	954	6	AR164148	AR164148 Sequence
8	1293	99.5	954	6	BD132528	BD132528 Ligand fo
9	1293	99.5	954	6	BD132534	BD132534 Receptor
10	1293	99.5	954	6	AR218282	AR218282 Sequence
11	1293	99.5	954	6	AR254111	AR254111 Sequence
12	1293	99.5	954	6	AR285410	AR285410 Sequence
13	1293	99.5	954	6	AR300119	AR300119 Sequence
14	1293	99.5	954	6	AR317339	AR317339 Sequence
15	1293	99.5	954	6	AR430237	AR430237 Sequence
16	1293	99.5	954	6	AX147989	AX147989 Sequence
17	1293	99.5	954	6	AX451895	AX451895 Sequence
18	1293	99.5	954	6	AX695691	AX695691 Sequence
19	1293	99.5	972	9	AB064270	AB064270 Homo sapi
20	1293	99.5	1003	9	BC074823	BC074823 Homo sapi
21	1293	99.5	1003	9	BC074890	BC074890 Homo sapi
22	1293	99.5	1034	9	AB064269	AB064269 Homo sapi
23	1293	99.5	1083	6	CQ725412	CQ725412 Sequence
24	1293	99.5	1561	9	BC040889	BC040889 Homo sapi
25	1293	99.5	2201	9	AF019047	AF019047 Homo sapi
26	1293	99.5	2226	6	AX695690	AX695690 Sequence
27	1293	99.5	2271	6	BD231044	BD231044 Method fo
28	1293	99.5	2271	6	AR429486	AR429486 Sequence
29	1293	99.5	2271	6	AX664282	AX664282 Sequence
30	1293	99.5	2271	9	AF053712	AF053712 Homo sapi
31	1293	99.5	2274	6	BD096827	BD096827 Osteoprot
32	1293	99.5	2390	6	AX201362	AX201362 Sequence
33	1108	85.3	1630	6	AR156433	AR156433 Sequence
34	1108	85.3	1630	6	AR164147	AR164147 Sequence
35	1108	85.3	1630	6	BD132527	BD132527 Ligand fo
36	1108	85.3	1630	6	BD132533	BD132533 Receptor
37	1108	85.3	1630	6	AR218281	AR218281 Sequence
38	1108	85.3	1630	6	AR254110	AR254110 Sequence
39	1108	85.3	1630	6	AR285409	AR285409 Sequence
40	1108	85.3	1630	6	AR300118	AR300118 Sequence
41	1108	85.3	1630	6	AR317338	AR317338 Sequence
42	1108	85.3	1630	6	AR430236	AR430236 Sequence
43	1108	85.3	1630	6	AX147987	AX147987 Sequence
44	1108	85.3	1694	6	AX451897	AX451897 Sequence
45	1108	85.3	2225	10	AF019048	AF019048 Mus muscu

Title: US-09-873-829-2  
Perfect score: 1299  
Sequence: 1 QMDPNRISEDGTHCIYRILR . . . . . LLDPDQDATYFGAFKVRDID 245

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09873829/runat_10032005_161838_26932/app_query.fasta_1
.391
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09873829_@CGN_1_1_708_@runat_10032005_161838_26932 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : N\_Geneseq\_16Dec04:\*
1: geneseqn1980s:\*
2: geneseqn1990s:\*
3: geneseqn2000s:\*
4: geneseqn2001as:\*
5: geneseqn2001bs:\*
6: geneseqn2002as:\*
7: geneseqn2002bs:\*
8: geneseqn2003as:\*
9: geneseqn2003bs:\*
10: geneseqn2003cs:\*
11: geneseqn2003ds:\*
12: geneseqn2004as:\*
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result      Query

No.	Score	Match	Length	DB	ID	Description
1	1299	100.0	1823	2	AAX80223	Aax80223 Human TRA
2	1299	100.0	1823	8	ABX94284	Abx94284 cDNA enco
3	1299	100.0	1823	8	ACC57900	Acc57900 Human RAN
4	1299	100.0	1823	10	ACC57571	Acc57571 Human RAN
5	1293	99.5	829	5	ABZ21473	Abz21473 Human sol
6	1293	99.5	930	10	ADC78864	Adc78864 Human PRO
7	1293	99.5	954	2	AAV69887	Aav69887 Nucleic a
8	1293	99.5	954	2	AAV41378	Aav41378 NF-kB rec
9	1293	99.5	954	2	AAV41372	Aav41372 NF-kB rec
10	1293	99.5	954	2	AAD15311	Aad15311 Human rec
11	1293	99.5	954	4	AAD08715	Aad08715 Human rec
12	1293	99.5	954	4	AAD05904	Aad05904 Human ful
13	1293	99.5	954	6	AAD43213	Aad43213 Human RAN
14	1293	99.5	954	7	ADR29335	Adr29335 Human RAN
15	1293	99.5	954	8	AAD52598	Aad52598 Human rec
16	1293	99.5	954	9	ADA02800	Ada02800 Human TNF
17	1293	99.5	954	9	ADB16987	Adb16987 Human rec
18	1293	99.5	954	10	ADB72538	Adb72538 Human TNF
19	1293	99.5	954	10	ADC73001	Adc73001 Human RAN
20	1293	99.5	954	10	ADC78267	Adc78267 Human RAN
21	1293	99.5	954	10	ADC85280	Adc85280 Human Tnf
22	1293	99.5	954	10	ADG46722	Adg46722 Human RAN
23	1293	99.5	954	12	ADM74395	Adm74395 Human car
24	1293	99.5	1931	12	ADO19773	Ado19773 Human PRO
25	1293	99.5	1945	6	ABK12877	Abk12877 cDNA enco
26	1293	99.5	2201	10	ACC57572	Acc57572 Human RAN
27	1293	99.5	2201	13	ADT08154	Adt08154 Human RAN
28	1293	99.5	2226	6	ABK12876	Abk12876 cDNA enco
29	1293	99.5	2226	9	ADA02799	Ada02799 Human TNF
30	1293	99.5	2226	10	ADB72537	Adb72537 Human TNF
31	1293	99.5	2226	10	ADC85279	Adc85279 Human Tnf
32	1293	99.5	2226	12	ADM74394	Adm74394 Human car
33	1293	99.5	2271	3	AAZ99964	Aaz99964 DNA encod
34	1293	99.5	2271	10	ADC35203	Adc35203 Human cDN
35	1293	99.5	2271	10	AAD63913	Aad63913 Human RAN
36	1293	99.5	2271	10	ABV75842	Abv75842 Human ost
37	1293	99.5	2274	2	AAV70285	Aav70285 Human ost
38	1293	99.5	2390	6	ABK40274	Abk40274 cDNA enco
39	1293	99.5	2390	10	ADJ37322	Adj37322 Human tum
40	1293	99.5	2390	12	ADG68246	Adg68246 Human PRO
41	1286	99.0	741	2	AAV69899	Aav69899 Nucleic a
42	1189	91.5	989	12	ADQ07631	Adq07631 Nucleotid
43	1108	85.3	1630	2	AAV41377	Aav41377 NF-kB rec
44	1108	85.3	1630	2	AAV41371	Aav41371 NF-kB rec
45	1108	85.3	1630	2	AAD15310	Aad15310 Murine re

Title: US-09-873-829-2  
Perfect score: 1299  
Sequence: 1 QMDPNRISEDGTHCIYRILR.....LLDPDQDATYFGAFKVRDID 245

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-  
Q=/cgn2\_1/USPTO\_spool\_p/US09873829/runat\_10032005\_161839\_26968/app\_query.fasta\_1  
.391  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09873829\_@CGN\_1\_1\_105\_@runat\_10032005\_161839\_26968 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:/\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:/\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:/\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:/\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:/\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:/\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
<hr/>						
1	1293	99.5	954	3	US-08-996-139-12	Sequence 12, Appl
2	1293	99.5	954	3	US-08-995-659-12	Sequence 12, Appl
3	1293	99.5	954	3	US-09-215-649A-12	Sequence 12, Appl
4	1293	99.5	954	3	US-09-577-780-12	Sequence 12, Appl
5	1293	99.5	954	4	US-09-577-800-12	Sequence 12, Appl

6	1293	99.5	954	4	US-09-466-496-12	Sequence 12, Appl
7	1293	99.5	954	4	US-09-871-856-12	Sequence 12, Appl
8	1293	99.5	954	4	US-09-871-291-12	Sequence 12, Appl
9	1293	99.5	954	4	US-09-877-650-12	Sequence 12, Appl
10	1293	99.5	954	4	US-09-865-363-12	Sequence 12, Appl
11	1293	99.5	954	4	US-09-688-459-12	Sequence 12, Appl
12	1293	99.5	2271	3	US-09-052-521C-3	Sequence 3, Appl
13	1293	99.5	2271	4	US-09-396-937-1	Sequence 1, Appl
14	1108	85.3	1630	3	US-08-996-139-10	Sequence 10, Appl
15	1108	85.3	1630	3	US-08-995-659-10	Sequence 10, Appl
16	1108	85.3	1630	3	US-09-215-649A-10	Sequence 10, Appl
17	1108	85.3	1630	3	US-09-577-780-10	Sequence 10, Appl
18	1108	85.3	1630	4	US-09-577-800-10	Sequence 10, Appl
19	1108	85.3	1630	4	US-09-466-496-10	Sequence 10, Appl
20	1108	85.3	1630	4	US-09-871-856-10	Sequence 10, Appl
21	1108	85.3	1630	4	US-09-871-291-10	Sequence 10, Appl
22	1108	85.3	1630	4	US-09-877-650-10	Sequence 10, Appl
23	1108	85.3	1630	4	US-09-865-363-10	Sequence 10, Appl
24	1108	85.3	1630	4	US-09-688-459-10	Sequence 10, Appl
25	1101	84.8	951	4	US-09-396-937-3	Sequence 3, Appl
26	1101	84.8	2191	3	US-08-989-362-1	Sequence 1, Appl
27	1101	84.8	2191	4	US-09-671-658A-1	Sequence 1, Appl
28	1101	84.8	2295	2	US-08-842-842-6	Sequence 6, Appl
29	1101	84.8	2295	3	US-09-052-521C-1	Sequence 1, Appl
30	1101	84.8	2299	4	US-09-396-937-5	Sequence 5, Appl
31	767	59.0	564	4	US-09-396-937-7	Sequence 7, Appl
32	765	58.9	519	4	US-09-396-937-9	Sequence 9, Appl
33	755	58.1	519	4	US-09-396-937-11	Sequence 11, Appl
34	717.5	55.2	564	4	US-09-396-937-13	Sequence 13, Appl
35	707.5	54.5	546	4	US-09-396-937-15	Sequence 15, Appl
36	687	52.9	519	4	US-09-396-937-17	Sequence 17, Appl
37	666	51.3	519	4	US-09-396-937-19	Sequence 19, Appl
38	235.5	18.1	759	3	US-09-320-424-10	Sequence 10, Appl
39	235.5	18.1	759	4	US-09-825-563-10	Sequence 10, Appl
40	235.5	18.1	768	3	US-09-320-424-12	Sequence 12, Appl
41	235.5	18.1	768	4	US-09-825-563-12	Sequence 12, Appl
42	234.5	18.1	1042	3	US-08-584-031-2	Sequence 2, Appl
43	234.5	18.1	1042	3	US-08-780-496-2	Sequence 2, Appl
44	234.5	18.1	1042	4	US-09-582-450-2	Sequence 2, Appl
45	234.5	18.1	1042	4	US-09-934-465-2	Sequence 2, Appl

Title: US-09-873-829-2  
Perfect score: 1299  
Sequence: 1 QMDPNRISEDGTHCIYRILR.....LLDPDQDATYFGAFKVRDID 245

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-  
Q=/cgn2\_1/USPTO\_spool\_p/US09873829/runat\_10032005\_161839\_26990/app\_query.fasta\_1  
.391  
-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09873829@CGN\_1\_1\_723@runat\_10032005\_161839\_26990  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1299	100.0	1823	10	US-09-873-829-1	Sequence 1, Appli
2	1299	100.0	1823	13	US-10-017-910-1	Sequence 1, Appli
3	1299	100.0	1823	15	US-10-272-411-1	Sequence 1, Appli
4	1299	100.0	1823	15	US-10-272-328A-1	Sequence 1, Appli
5	1299	100.0	1823	17	US-10-202-062-21	Sequence 21, Appli
6	1293	99.5	741	16	US-10-167-182-19	Sequence 19, Appli
7	1293	99.5	741	17	US-10-460-623-19	Sequence 19, Appli
8	1293	99.5	741	18	US-10-854-300-19	Sequence 19, Appli
9	1293	99.5	954	9	US-09-871-856-12	Sequence 12, Appli
10	1293	99.5	954	9	US-09-957-944-5	Sequence 5, Appli
11	1293	99.5	954	9	US-09-865-363-12	Sequence 12, Appli
12	1293	99.5	954	9	US-09-871-291-12	Sequence 12, Appli
13	1293	99.5	954	9	US-09-877-650-12	Sequence 12, Appli
14	1293	99.5	954	11	US-09-997-722-66	Sequence 66, Appli
15	1293	99.5	954	14	US-10-151-071-9	Sequence 9, Appli
16	1293	99.5	954	16	US-10-405-878-12	Sequence 12, Appli
17	1293	99.5	954	16	US-10-167-182-12	Sequence 12, Appli
18	1293	99.5	954	17	US-10-460-623-12	Sequence 12, Appli
19	1293	99.5	954	18	US-10-802-133-12	Sequence 12, Appli
20	1293	99.5	954	18	US-10-854-300-12	Sequence 12, Appli
21	1293	99.5	1945	11	US-09-933-915A-9	Sequence 9, Appli
22	1293	99.5	2201	15	US-10-272-411-51	Sequence 51, Appli
23	1293	99.5	2201	15	US-10-272-328A-51	Sequence 51, Appli
24	1293	99.5	2201	18	US-10-799-345-11	Sequence 11, Appli
25	1293	99.5	2226	11	US-09-997-722-65	Sequence 65, Appli
26	1293	99.5	2226	11	US-09-933-915A-1	Sequence 1, Appli
27	1293	99.5	2271	15	US-10-218-547-21	Sequence 21, Appli
28	1293	99.5	2271	16	US-10-310-793-27	Sequence 27, Appli
29	1293	99.5	2271	18	US-10-664-801-1	Sequence 1, Appli
30	1293	99.5	2271	18	US-10-825-898-3	Sequence 3, Appli
31	1293	99.5	2271	19	US-10-129-595-2	Sequence 2, Appli
32	1293	99.5	2390	16	US-10-210-951-41	Sequence 41, Appli
33	1293	99.5	2390	16	US-10-211-884-41	Sequence 41, Appli
34	1293	99.5	2390	17	US-10-211-858-41	Sequence 41, Appli
35	1108	85.3	1630	9	US-09-871-856-10	Sequence 10, Appli
36	1108	85.3	1630	9	US-09-865-363-10	Sequence 10, Appli
37	1108	85.3	1630	9	US-09-871-291-10	Sequence 10, Appli
38	1108	85.3	1630	9	US-09-877-650-10	Sequence 10, Appli
39	1108	85.3	1630	16	US-10-405-878-10	Sequence 10, Appli
40	1108	85.3	1630	18	US-10-802-133-10	Sequence 10, Appli
41	1108	85.3	1694	9	US-09-957-944-7	Sequence 7, Appli
42	1108	85.3	2225	18	US-10-799-345-9	Sequence 9, Appli
43	1101	84.8	735	16	US-10-167-182-18	Sequence 18, Appli
44	1101	84.8	735	17	US-10-460-623-18	Sequence 18, Appli
45	1101	84.8	735	18	US-10-854-300-18	Sequence 18, Appli

Title: US-09-873-829-2  
Perfect score: 1299  
Sequence: 1 QMDPNRISEDGTHCIYRILR.....LLDPDQDATYFGAFKVRDID 245

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09873829/runat_10032005_161838_26951/app_query.fasta_1
.391
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09873829@CGN_1_1_5180@runat_10032005_161838_26951 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_htc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
	No.	Score	Match	Length	DB	
1	1293	99.5	954	9	AY415854	AY415854 Homo sapi
2	1271	97.8	735	9	AY415855	AY415855 Pan trogl

	3	1047	80.6	951	9	AY415856	AY415856 Mus muscu
	4	741	57.0	670	9	CE649975	CE649975 tigr-gss-
c	5	682	52.5	612	8	BH267783	BH267783 CH230-186
c	6	630	48.5	694	9	AG319098	AG319098 Mus muscu
	7	563	43.3	362	1	AV653073	AV653073 AV653073
c	8	516	39.7	725	9	AG484312	AG484312 Mus muscu
	9	453	34.9	855	5	BX843917	BX843917 BX843917
	10	450	34.6	659	9	AG107545	AG107545 Pan trogl
c	11	426	32.8	524	8	AQ827122	AQ827122 HS_5256_B
	12	423	32.6	688	6	BY753873	BY753873 BY753873
	13	397	30.6	599	7	CK823311	CK823311 ij28a04.y
	14	385	29.6	671	6	BY754477	BY754477 BY754477
	15	367.5	28.3	933	6	CA982721	CA982721 AGENCOURT
	16	358	27.6	572	5	BM966907	BM966907 ij28a04.y
c	17	354.5	27.3	889	5	BX772925	BX772925 BX772925
	18	344	26.5	918	6	CA971751	CA971751 AGENCOURT
c	19	339.5	26.1	529	8	AQ827168	AQ827168 HS_5256_B
	20	279	21.5	671	6	BY753653	BY753653 BY753653
	21	270	20.8	609	2	BF427340	BF427340 df64e08.y
	22	248	19.1	618	8	AZ834036	AZ834036 2M0116G04
	23	238.5	18.4	846	9	AY408451	AY408451 Pan trogl
	24	237.5	18.3	1084	7	CN642403	CN642403 ILLUMIGEN
c	25	235	18.1	792	7	CK769375	CK769375 956956 MA
	26	234.5	18.1	846	9	AY408450	AY408450 Homo sapi
	27	234.5	18.1	996	5	BX399299	BX399299 BX399299
	28	234.5	18.1	1018	1	AL547417	AL547417 AL547417
	29	234.5	18.1	1135	1	AL543620	AL543620 AL543620
	30	234.5	18.1	1640	3	CR598109	CR598109 full-leng
	31	234.5	18.1	1688	3	CR594331	CR594331 full-leng
	32	234	18.0	876	9	AY408452	AY408452 Mus muscu
	33	233.5	18.0	976	7	CO649111	CO649111 ILLUMIGEN
c	34	232.5	17.9	662	5	BM968547	BM968547 UI-CF-DU1
	35	232.5	17.9	984	5	BX382031	BX382031 BX382031
	36	232.5	17.9	1044	5	BX380980	BX380980 BX380980
c	37	231.5	17.8	662	6	CB305927	CB305927 UI-CF-EN1
	38	231.5	17.8	928	6	CD516251	CD516251 AGENCOURT
	39	230	17.7	571	6	CB444606	CB444606 695786 MA
c	40	230	17.7	717	6	CB438089	CB438089 686530 MA
	41	225	17.3	413	8	AQ817650	AQ817650 HS_5265_B
c	42	225	17.3	519	5	BQ013887	BQ013887 UI-1-BC1p
	43	225	17.3	683	2	AW949689	AW949689 EST361759
	44	225	17.3	718	2	AW945165	AW945165 EST361358
	45	225	17.3	1071	5	BX424920	BX424920 BX424920